

CC expression of the polypeptide. Antagonists, inhibitory nucleic acid or
 CC competitive polypeptide are useful for inhibiting the polypeptide e.g.
 CC bacterial (especially *S. aureus*) infections. They are also useful against
 CC Helicobacter pylori infections and related cancers, ulcers and gastritis.
 CC The antibacterial agents are useful to treat in-dwelling devices for
 CC infection prevention or generally as wound treatments to prevent adhesion
 CC of bacteria to matrix proteins. The MurC polypeptide is also useful for
 CC diagnosing or prognosing a (susceptibility to) disease, for raising
 CC antibodies, to identify modulators or specific receptors; in rational
 CC drug design and as an immunogen for vaccines. The MurC gene sequences are
 CC useful in antisense/ribozyme therapeutics; to detect mutant MurC gene;
 CC for chromosomal mapping; to determine bacterial serotype; and for genetic
 CC immunisation.

SQ Sequence 1351 BP; 471 A; 166 C; 260 G; 454 T;

Query Match 98.4%; Score 5363; DB 60; Length 1351;

Best Local Similarity 60.9%; Pred. No. 0.00e+00;

Matches 799; Conservative 320; Mismatches 192; Indels 0; Gaps 0;

Db 22 atgacacatcatcttctgcgaataaaggtcttgcgcatgattcattacacaaatc 81

QY 1 ATGACNCAYTAYCAVTTGTGNGNATHAARGGNWSNGNATGWSNWSNTGNCNCARATH 60

Db 82 atgcattgtaggaacatgaattcaagatcggaattggaactacattattacaga 141

QY 61 ATGCAYGAYTTGNGNCAYGARGTNCARGGNWSNGAYATHGARAAYTAYGTNTTYACNGAR 120

Db 142 gttgctcttagaaaagaagggataaaatattaccattgttgctaaatacaataaaga 201

QY 121 GTGNCNTYTNWNAAYARGGNATHARATHYNTCCNTYTGNGNCNAAYAYATHAARGAR 180

Db 202 gatattgtagttatcaaggtatgcatcgogagtagocatgaagaataagtagctgca 261

QY 181 GAYATGCTGNTGTHCARGGNAAAGTNTYGCNWSNWSNCAYGARGARATHGTMNGNCGN 240

Db 262 catcaattgaaatagattgttaagtataatgatttttttaggcagagattattgataa 321

QY 241 CAYCARYTNAARYTNGAYGTGNTGNTWSNTAYAYGATYTTTNGNCGARATHATHGAYCAR 300

Db 322 tatacttcagtagcttaactgtgcacatggttaaaacttctacaacaggtttattatca 381

QY 301 TAYACNWSNGTNCNGTNCACNGGNCAYGNAARACNWSNACNACNGNTYTNWSN 360

Db 382 catgttatgaatggtgataaaaagaacttcttttaattggtgtaggcacaggtatggga 441

QY 361 CAYGTNATGAAYGNGAYAAARACNWSNTYTNATHGNGAYGNGNACNGNATGGGN 420

Db 442 ttgctgaaagtagattatttcgcttttttaggcagatgtaatatagacgctcattttaagt 501

QY 421 YTNCCNGARWSNGAYTAYTTGCTNTYTGAGCTGTGARTAYMNGNNGNCAYTTTYTNWSN 480

Db 502 tataaacctgattacgcaaatatgacaaattgattgctcatctgattattttcaaa 561

QY 481 TAYAAACCNGAYTAYCGNATHATGACNAAYATHGAYTTTAYCAYCCNGAYTAYTYAAR 540

Db 562 gatattaatgatgtttttgattcccaagaataatggcacaataatgttaaaaaaggtatt 621

QY 541 GAYATHAAYGAYGNTTYGAYGCTTYTCARGARATGCGNCAYAAAYGTNNAARAARGGNATH 600

Db 622 attgctggggtgatgatgaacatctacgtataaatgaagcagatgttccaaattttac 681

QY 601 ATHGCTNTGGGNGAYGAYGARGAYTNNMNAARATHGARGCNGAYGTNCCNAYTHAYTAY 660

Db 682 tatgatttaaaagattcggtacattatgctcaaaatattcaaatcaggtataaaggt 741

QY 661 TAYGNTTYAARGYWSNGAYGAYATHATAYCCNARAYATHARATHACNGAYAARGGN 720

Db 742 actgctttgatgtgattggtgatttttatgatcactctctgtctccacaatat 801

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Db 802 ggtgacacatacagtttaaatgattagctgtaattgcgattagttatttagagaagcta 861

QY 781 GGNAYCAYACNGTNTYNAAYGCNTYNGCNGTNGATHGNCNATHWSNTAYTYTNGARAARYTN 840

Db 862 gatgttacaataattaaagaagcattagaaacgcttgggtggttaaacgctgtttcaat 921

QY 841 GAYGTNACNAAYATHAARGARGCNTYNGARACNTYGGGNGCNTYNAARMNGNTTYAAY 900

Db 922 gaactacaattgcaaatcaagttattgattatgacacaccatccaagaagaatt 981

QY 901 GARACNACNATHGNCNAAYCARGTNNATHGNTNGAYGAYTAYGNCNAYCAYCCNMGNGARATH 960

Db 982 agtgcataattgacacagcagcaaaataatccacataaagaagttgttgcagatttt 1041

QY 961 WSNCGNACNATHGAYACNCGNMGNAARAARTAYCCNCAAYAAARGARGTNGTNGCNGTNTTY 1020

Db 1042 caaacacacactttctctagaacacacacgatttttaataatgaatttcgagaaagttaagt 1101

QY 1021 CARCCNCAVACNTTYTWSNMGNCNACARGCNTTYTNAAYGARTTYGCGNARWSNTYNTGY 1080

Db 1102 aaagcagatcgtattcttattgtgaaatttttgctcaattagagaaaattctggcgca 1161

QY 1081 AARGCNGAYMNGTNTTYTNGYGARATHHTTYGNGNATHMNGARAAYWSNNGNCGN 1140

Db 1162 ttaacgatacagaatttaattgataaaattggagtgatcgttcttataatgaagatttt 1221

QY 1141 YTNACNATHCARGAYTNTATHGAYAAATHGNGGNGCNGWSNTTYATHAAYGARGAYTN 1200

Db 1222 ataatgtattagaacaatttgataatcgtgtgtttttatttattggtgaggtgatatt 1281

QY 1201 ATHAAYGNTYTNAGARCARTTYGAYAYGCTGNTGNTYNTTYATGGGNGCNGGAYATH 1260

Db 1282 caaaaattcaaaaatgcattattagataaatttagcattagcaaaaatgcggttt 1332

QY 1261 CARAARYTNCAARAAYTNTAYTYTNGAYAARYTNGNATGAARAAYGCNTTY 1311

RESULT 2

ID V74703 standard; DNA; 2424 BP.

AC V74703;

DT 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #392.

KW Computer readable medium; vaccine; S.aureus infection; Immunodetection;

KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

KW skin infection; surgical wound infection; scalded skin syndrome;

KW toxic shock syndrome; ds.

OS Staphylococcus aureus.

FH Key Location/Qualifiers

FT misc_feature 1141..1200

FT /*tag= a

FT /note= "these bases represent a line of missing text in

the sequence listing in the specification. They

are included to maintain the nucleotide numbering

given in the specification for this DNA sequence"

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EP-786519-A2.
 30-JUL-1997.
 07-JAN-1997; 100117
 05-JAN-1996; US-009861.
 (HUMA-) HUMAN GENOME SCI INC.
 Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
 Rosen CA;
 WPI; 97-374922/35.
 Polynucleotide(s) and proteins derived from *Staphylococcus aureus*
 stored on computer readable medium and used in the production of
 anti-S.aureus vaccines
 Claim 1; Page 1287-1288; 3271pp; English.
 This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences
 of the invention. The DNA sequences are recorded on a computer readable
 medium, preferably selected from a floppy or hard disk, random access
 memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 the S.aureus DNA sequences allows putative functions to be assigned so
 that protein-encoding or regulatory regions of commercial, therapeutic or
 industrial importance can be obtained. Specifically, sequences which are
 likely to encode antigens have been identified and these polypeptides can
 be used in a vaccine composition against *S.aureus* infection. The

[illegible]

claim 2, pages 4-5, 38pp, English.
The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoded by the *S. aureus* MurC gene. Host cells containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially *S. aureus*) infections. They are also useful against *Helicobacter pylori* infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adherence of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or proposing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant MurC genes

 M I S R L H

 (TM)

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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
 Run on: Sat Nov 27 12:32:46 1999; MasPar time 162.98 Seconds
 Tabular output not generated. 867.701 Million cell updates/sec
 Title: >US-09-103-287-3
 Description: (1-660) from US09103287.seq
 Perfect Score: 660
 N.A. Sequence: 1 ATTTAAAGATTCGGATGACA.....CGCTTTTAATATGTTTATAA 660
 Comp: TAAATTTCTAAGCCTACTGT.....CGCAAAATTATACAAATTT
 Scoring table: TABLE default
 Gap 6
 Nmatch STD : Dbase 0; Query 0
 Searched: 271905 seqs, 107135622 bases x 2
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: n-geneseq35
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39 40:part40 41:part41 42:part42 43:part43
 44:part44 45:part45 46:part46 47:part47 48:part48
 49:part49 50:part50 51:part51 52:part52 53:part53
 54:part54 55:part55 56:part56 57:part57 58:part58
 59:part59 60:part60

Statistics: Mean 8.484; Variance 6.123; scale 1.386

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.	
1	646	97.9	2424	58	Staphylococcus aureus	0.00e+00	
2	638	96.7	660	60	Partial nucleotide se	0.00e+00	
3	638	96.7	1351	60	UDP-N-acetylmutamate	0.00e+00	
c	4	587	88.9	619	DNA encoding a Staphy	0.00e+00	
5	111	16.8	677	60	Enterococcus faecalis	1.41e-45	
6	92	13.9	1267	45	Streptococcus pneumonia	5.16e-35	
c	7	92	13.9	1267	45	Streptococcus pneumonia	5.16e-35
c	8	80	12.1	1825	47	Streptococcus pneumonia	1.94e-28
c	9	38	5.8	91	9	Oligonucleotide probe	1.37e-06

c	10	37	5.6	204	1	N81164	Base substituted E.co	4.14e-06
c	11	36	5.5	204	1	N81164	Base substituted E.co <td>1.24e-05</td>	1.24e-05
c	12	34	5.2	91	9	O51746	Oligonucleotide probe <td>1.09e-04</td>	1.09e-04
c	13	34	5.2	114	12	Q70466	Generic DNA sequence <td>1.09e-04</td>	1.09e-04
c	14	33	5.0	91	46	V44650	Mammalian DNA replica <td>3.18e-04</td>	3.18e-04
c	15	32	4.8	114	12	Q70468	Mammalian DNA replica <td>9.22e-04</td>	9.22e-04
c	16	32	4.8	114	12	Q70468	Generic DNA sequence <td>9.22e-04</td>	9.22e-04
c	17	32	4.8	114	12	Q70465	Generic DNA sequence <td>9.22e-04</td>	9.22e-04
c	18	32	4.8	114	12	Q70469	Generic DNA sequence <td>9.22e-04</td>	9.22e-04
c	19	32	4.8	114	12	Q70467	Generic DNA sequence <td>9.22e-04</td>	9.22e-04
c	20	26	3.9	114	12	Q70468	Generic DNA sequence <td>4.33e-01</td>	4.33e-01
c	21	26	3.9	498	3	N50034	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	22	26	3.9	501	3	N50032	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	23	26	3.9	501	3	N50029	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	24	26	3.9	501	3	N50028	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	25	26	3.9	501	3	N50026	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	26	26	3.9	501	3	N50030	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	27	26	3.9	501	3	N50034	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	28	26	3.9	501	3	N50033	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	29	26	3.9	501	3	N50031	Sequence encoding new <td>4.33e-01</td>	4.33e-01
c	30	25	3.8	114	12	Q70465	Generic DNA sequence <td>1.15e+00</td>	1.15e+00
c	31	25	3.8	114	12	Q70467	Generic DNA sequence <td>1.15e+00</td>	1.15e+00
c	32	25	3.8	114	12	Q70469	Generic DNA sequence <td>1.15e+00</td>	1.15e+00
c	33	25	3.8	501	3	N50027	Sequence encoding new <td>1.15e+00</td>	1.15e+00
c	34	25	3.8	501	3	N50030	Sequence encoding new <td>1.15e+00</td>	1.15e+00
c	35	25	3.8	501	3	N50025	Sequence encoding new <td>1.15e+00</td>	1.15e+00
c	36	25	3.8	1200	2	Q10187	Sequence encoding fun <td>1.15e+00</td>	1.15e+00
c	37	24	3.6	39	7	Q51787	Mixed oligonucleotide <td>3.02e+00</td>	3.02e+00
c	38	24	3.6	108	23	T29064	Probe for Candida alb <td>3.02e+00</td>	3.02e+00
c	39	24	3.6	114	12	Q70470	Generic DNA sequence <td>3.02e+00</td>	3.02e+00
c	40	24	3.6	146	21	T13624	ME#2b library generat <td>3.02e+00</td>	3.02e+00
c	41	24	3.6	1440	26	T28571	Bacterial antibiotic <td>3.02e+00</td>	3.02e+00
c	42	24	3.6	1676	60	X13557	Enterococcus faecalis <td>3.02e+00</td>	3.02e+00
c	43	24	3.6	2171	1	N61688	Sequence of part of t <td>3.02e+00</td>	3.02e+00
c	44	24	3.6	2403	21	T12562	S.aureus topoisomeras <td>3.02e+00</td>	3.02e+00
c	45	24	3.6	2403	21	T12573	S.aureus mutant gria <td>3.02e+00</td>	3.02e+00

ALIGNMENTS

RESULT 1
 ID V74703 standard; DNA; 2424 BP.
 AC V74703;
 DT 16-MAR-1999 (first entry)
 DE Staphylococcus aureus contig SEQ ID #392.
 KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
 KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 KW skin infection; surgical wound infection; scalded skin syndrome;
 KW toxic shock syndrome; ds.
 OS Staphylococcus aureus.
 FH Key Location/Qualifiers
 FT misc_feature 1141..1200
 FT /*tag=a
 FT /note= *these bases represent a line of missing text in
 the sequence listing in the specification. They
 are included to maintain the nucleotide numbering
 given in the specification for this DNA sequence"
 PN EP-786519-A2.
 PD 30-JUL-1997.
 PE 07-JAN-1997; 100117.
 PR 05-JAN-1996; US-009861.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
 PI Rosen CA;
 DR WPI; 97-374922/35.
 PT Polynucleotide(s) and proteins derived from Staphylococcus aureus
 stored on computer readable medium and used in the production of
 anti-S.aureus vaccines
 PS Claim 1; Page 1287-1288; 3271pp; English.
 CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 of the invention. The DNA sequences are recorded on a computer readable
 medium, preferably selected from a floppy or hard disk, random access
 memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using

CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S.aureus DNA sequences contained on the
 CC computer readable medium.

Sequence 2424 BP; 839 A; 302 C; 462 G; 759 T;

Query Match 97.9%; Score 646; DB 58; Length 2424;

Best Local Similarity 98.9%; Pred. No. 0.00e+00;

Matches 653; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Db 1292 atttaagattcggatgacatttatctcaaaatattcaaaattacggataaagggtactgc 1351

QY 1 ATTAAAGATTCCGGATGACATTATCTCAATATATTTCAAATTACGGATAAAGGTACTGC 60

Db 1352 ttttgatggtatggtatggtggtttttatgatcacttcctgtctccacaatatggtga 1411

QY 61 TGTGTATGTATGTGGATGGTGGATTTTATGATCATCTTCTGTCTCCACAATATGGTGA 120

Db 1412 ccatacagtttttaaaatgattgctgtaattcgatttagtttttagagaactagatgt 1471

QY 121 CCATACAGTTTAAAGTGCATTAGCTGTAATGCGATTAGTTATTTAGAGAAGCTAGATGT 180

Db 1472 tacaaatattaaagaagcattgaaacgtttgtgtgtgttaaacgttcgttcaatgaac 1531

QY 181 TACAATATTAAAGACATTAGAACGTTTGGTGTGTAAACGTCGTTTCAATGAAC 240

Db 1532 tacaattgcaaatcaagtttattgtatgattatgcacaccatcccaagagaattagtg 1591

QY 241 TACAATGCAAAATCAAGTTATTGTATGATTATGACACACCATCCAAAGAGAATATAGTC 300

Db 1592 tacaattgaaacagcagaaagaataatccacataaagaagttgttgcaatttcaaac 1651

QY 301 TACAATTGACACAGCAGCAAGAAATATCCATAAAGAAGTTGTTGCGATATTCAACC 360

Db 1652 acacatttctctagacacagcagcatttttaaatgaattgcagaaagtttaagtaaac 1711

QY 361 ACACACTTCTCTAGAACACAGCATTTTAAATGATTTGCGAGAAGTTTAAGTAAC 420

Db 1712 agatcgtgtattcttattgtgaatttttggatcatttagagaaaatactggcgattaac 1771

QY 421 AGATCGTGTATTCTTATGTGAAATTTTGGATCAATTAGAGAAAATCTGCGCATTAAC 480

Db 1772 gatacaagatttaattgataaattgaaggtcagtcgttaataatgaagattcattaa 1831

QY 481 GATACAGAAATTAAATTGATAAATTGAAGGTGCATCGTTAAATTAATGAAGATTCATTAA 540

Db 1832 tgtattagacaatttgataatgcgttattttatttattgggtgcaggtgattcaaaa 1891

QY 541 TGTATTAGAACAAATTGATAAATGCTGTTGTTTATTATGTTGGTGCAGGTGATATCAAAA 600

Db 1892 attacaaaatgcatttttagataaatttagcgatgaaaatgcgttttaattatttttaa 1951

QY 601 ATTACAAAATGCATATTATAGATAAATTAGGCATGAATAAATGCGTTTAAATATGTTTAA 660

RESULT

ID V80065 standard; DNA; 660 BP.

AC V80065;

DT 17-MAR-1999 (first entry)

DE Partial nucleotide sequence of the MurC gene.

KW MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;

KW bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine;

KW immunogen; drug; genetic immunisation; ds.

OS Staphylococcus aureus.

FH Key Location/Qualifiers

FT CDS 2..660

FT /tag- a

FT /product= "partial MurC polypeptide"

PN EP-889123-A2.

PD 07-JAN-1999.

PR 26-JUN-1998; 305064.

PA (SMK) SMITHKLINE BEECHAM CORP.

PA (SMK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Wallis NG;

DR P-PSDB; W89199.

DR WPI; 99-062655/06.

PT New isolated MurC polypeptide from Staphylococcus aureus and related

PT nucleic acid - useful in diagnosis, treatment and prevention of

PT bacterial infections

PS Claim 2; Pages 4-5; 39pp; English.

CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase

CC (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells

CC containing an expression system comprising the MurC gene can be used for

CC the recombinant production of the polypeptide. Agonists or the MurC

CC polypeptide are used to treat conditions requiring increased activity or

CC expression of the polypeptide. Antagonists, inhibitory nucleic acid or

CC competitive polypeptide are useful for inhibiting the polypeptide e.g.

CC bacterial (especially S. aureus) infections. They are also useful against

CC Helicobacter pylori infections and related cancers, ulcers and gastritis.

CC The antibacterial agents are useful to treat in-dwelling devices for

CC infection prevention or generally as wound treatments to prevent adhesion

CC of bacteria to matrix proteins. The MurC polypeptide is also useful for

CC diagnosing or prognosing a (susceptibility to) disease, for raising

CC antibodies; to identify modulators or specific receptors; in rational

CC drug design and as an immunogen for vaccines. The MurC gene sequences are

CC useful in antisense/ribozyme therapeutics; to detect mutant MurC gene;

CC for chromosomal mapping; to determine bacterial serotype; and for genetic

CC immunisation. The present sequence represents a partial nucleotide

CC sequence (MurC ORF) of the MurC gene.

QY Sequence 660 BP; 233 A; 120 G; 224 T;

Query Match 96.7%; Score 638; DB 60; Length 660;

Best Local Similarity 98.3%; Pred. No. 0.00e+00;

Matches 649; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 1 atttaagattcggatgacatttatctcaaaatattcaaaattacggataaagggtactgc 60

QY 1 ATTAAAGATTCCGGATGACATTATCTCAATATATTTCAAATTACGGATAAAGGTACTGC 60

Db 61 ttttgatggtatggtggtggtttttatgatcacttcctgtctccacaatatggtga 120

QY 61 TGTGTATGTATGTGGATGGTGGATTTTATGATCATCTTCTGTCTCCACAATATGGTGA 120

Db 121 ccatacagtttttaaaatgattgctgtaattcgatttagtttttagagaactagatgt 180

QY 121 CCATACAGTTTAAAGTGCATTAGCTGTAATGCGATTAGTTATTTAGAGAAGCTAGATGT 180

Db 181 tacaataattaaagaagcattagaaacgtttgtgtgttttaaacgtctttcaatgaac 240

QY 181 TACAATATTAAAGNAGCATTTAGAAACGTTTGGTGGTGTAAACGTCGTTTCAATGAAC 240

Db 241 tacaattgcaaatcaagtttattgtatgatttagtcacaccatcccaagagaattagtg 300

QY 241 TACAATTGCAAAATCAAGTTATTGTATGATTATGACACACCATCCCAAGAGAAATAGTGC 300

Db 301 tacaattgacacagcagaaagaataatccacataaagaagttgttgcaagtatttcaacc 360

QY 301 TACAATTGACACAGCAGCAAGAAATAATCCACATAAAGAAGTTGTTGCAGTATTTCACAC 360

Db 361 acacatttctctagacacacacagcatttttaaatgaatttcagaaagtttatgtgaaagc 420

QY 361 ACACACTTCTCTAGACACACAGCATTTTAAATGAATTTGCAGAAAGTTTAAGTAAC 420

Db 421 agatcgtgtattcttattgtgaaatttttggctcaattagagaataattctggcgattaac 480

QY 421 agatcgtgtattcttattgtgaaatttttggctcaattagagaataattctggcgattaac 480

W P S R L H

(TM)

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MPsrch_tpn n.a. n.a. Smith-Waterman search, using a protein query
which has been backtranslated into n.a. using IUPAC symbols

Run on: Sat Nov 27 10:20:03 1999; MasPar time 159.66 Seconds
Tabular output not generated. 865.603 Million cell updates/sec

Title: >US-09-103-287-4
Description: (J-215) from US09103287.pep
Perfect Score: 2663
N.A. Sequence: 1 TTYAARGAYWSNGAYGAYAT.....TNGGNATGAARAAYGCNTTY 645
Comp: AARTTYCTRWSCNCTRTA.....ANCCNCTACTYTTTGCGAAR

Scoring table: TABLE bktranslated2
Gap 30

Nmatch STD : Dbase 0; Query 0

Searched: 271905 seqs, 107135622 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
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19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part43
44:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part54 55:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 50.914; Variance 239.321; scale 0.213

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description	Pred. No.
1	2573	96.6	2424	58	Staphylococcus aureus	3.53e-212
2	2557	96.0	660	60	Partial nucleotide se	9.99e-211
3	2557	96.0	1351	60	UDP-N-acetylmuramate	9.99e-211
4	2329	87.5	619	48	DNA encoding a Staphy	4.65e-190
5	934	35.1	677	60	Enterococcus faecalis	4.66e-65
6	749	28.1	1267	46	Streptococcus pneumoniae	6.67e-49
7	749	28.1	11864	47	Streptococcus pneumoniae	6.67e-49
8	699	26.2	1825	47	Streptococcus pneumoniae	1.42e-44

H. pylori cytoplasmic 2.48e-05
H. pylori cytoplasmic 2.48e-05
H. pylori cytoplasmic 7.08e-04
Streptococcus pneumoniae 1.57e-02
Streptococcus pneumoniae 1.57e-02
Streptococcus pneumoniae 1.57e-02
S. pneumoniae MurD MR 1.57e-02
S. pneumoniae MurD MR 1.57e-02
DNA encoding S. pneum 1.57e-02
Streptococcus pneumoniae 1.57e-02
Degenerate nucleotide 1.98e+00
Synthetic HIV gag gen 2.30e+00
Sequence encoding new 1.17e+01
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Degenerate human tumo 1.01e+01
Human gelsolin gene c 1.56e+01
Sequence encoding N-t 1.35e+01
H. pylori cytoplasmic 2.41e+01
Pseudomonas fluoresce 2.41e+01
Heat shock protein (H 1.81e+01
Sequence encoding new 3.21e+01
Human Interleukin-XX 2.78e+01
Degenerate Alteromona 3.70e+01
Sequence encoding mat 3.70e+01
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Sequence of a cDNA en 3.70e+01
Colony stimulating fa 3.70e+01
Gene for human colony 3.70e+01
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Human short form CSF- 3.70e+01
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Human colony stimulat 3.70e+01
Partial PCR fragment 3.70e+01
Sequence of clone lam 3.70e+01
Enterococcus faecalis 3.70e+01
Enterococcus faecalis 2.78e+01

ALIGNMENTS

RESULT 1
ID V74703 standard; DNA; 2424 BP.
AC V74703;
DE 16-MAR-1999 (first entry)
KW Staphylococcus aureus contig SEQ ID #392.
KW Computer readable medium; vaccine; S aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW skin infection; surgical wound infection; scalded skin syndrome;
KW toxic shock syndrome; ds.
OS Staphylococcus aureus.
FH Key Location/Qualifiers
FT misc_feature 1141..1200
FT /*tag-a

FT /note- "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"

EP-786519-A2.

30-JUL-1997.

07-JAN-1997; 100117.

05-JAN-1996; US-009861.

(HUMA-) HUMAN GENOME SCI INC.

Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,

Rosen CA;

WPI; 97-374922/35.

Polynucleotide(s) and proteins derived from Staphylococcus aureus

stored on computer readable medium and used in the production of

anti-S aureus vaccines

Claim 1; Page 1287-1288; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences
of the invention. The DNA sequences are recorded on a computer readable
medium, preferably selected from a floppy or hard disk, random access

CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the S.aureus DNA sequences contained on the
 CC computer readable medium.

SQ Sequence 2424 BP; 839 A; 302 C; 462 G; 759 T;

Query Match 96.6%; Score 2573; DB 58; Length 2424;

Best Local Similarity 59.5%; Pred. No. 3,538-212;

Matches 384; Conservative 158; Mismatches 103; Indels 0; Gaps 0;

Db 1293 tttaaagattcgatgacattttatgctcaaaattacacgataaaggtagctt 1352

QY 1 TTYAARGAWSNGAYGAYATHYAGCNCARATHYTCARATHACNGAYAARGNACNGCN 60

Db 1353 ttgtatgtatgtggtgagttttatgatcacttctctccacaattatggtgac 1412

QY 61 GTNGAYGTNTAYGTNGAYGNGARTTYTAYGAYCAVTTYTNWSNCCNARTAYGNGAY 120

Db 1413 catacagttttaaattcattagctgaattgagtagtatttagagaagtagatgtt 1472

QY 121 CAYACNGTNTNAYGNGTNGCNGTNGTNGCNGTNGTNGTNGTNGTNGTNGTNGTNG 180

Db 1473 acaaaattaaagaacattagaaacgtttgtgtggttaaacgtcttcaatgaact 1532

QY 181 ACNAAATHAARGARCNCTNGARACNTTYGNGGNGTNGTNGTNGTNGTNGTNGTNGTNG 240

Db 1533 acaattgcaatacaagttatttagatgattgacacaccatccagaagaattagtt 1592

QY 241 ACNATHGCAACARGTATGTHGTNGAYGAYTAYGNCAYCAYCCNMGNGARATHWSN 300

Db 1593 acaattgcaacagcagaagaataatcacataaagaattgttgagtagtattcaacca 1652

QY 301 ACNATHGAYACNGCNGMNGNARARTAYCCNAYARGARTNGTNGCNGTNTTYCARCCN 360

Db 1653 cacacttctctagacacagcagctttttaaattgattgacagaagtttaagtaagca 1712

QY 361 CAYACNTTWSNMGNCARCNCTTYTNTNAYGARTTYGNGARWSNTNWSNARCN 420

Db 1713 gatcgtgatttcttattgtgaaatttttgatcaattagagaataactggcgacattaag 1772

QY 421 GAYMGNTTNTTYTNGYCARATHYTCGNGSNATHMGNGARAAVACNGGNGCNTNACN 480

Db 1773 atacaagatttattgataaaattgaagtgatcgttatttaataagaagattctattat 1832

QY 481 ATHCARGAYTNTATHGAYAAATHGARGGNGCNGSNATHNATTAAGAYGAYSNATHAY 540

Db 1833 gtattagaacaattgataactgctgttatttatttattggtgaggtgatattcaaaaa 1892

QY 541 GTNYTNGARCACTTYGAYAAAYGNGTNGTNGTNTTYTATGGGNGCNGGNGAYATHCARAR 600

Db 1893 ttcaaaaatgcattatttagataaattagcagataaaatgcgttt 1937

QY 601 YTNCAARAAYGCTNTAYTNGAYAAAYTNGCNGATGAARAAYGCTNTY 645

RESULT 2

ID V80065 standard; DNA; 660 BP.

AC V80065;

DT 17-MAR-1999 (first entry)

DE Partial nucleotide sequence of the MurC gene.

KW MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide;

KW immunogen; drug; genetic immunisation; ds.
 OS Staphylococcus aureus.

PH Key Location/Qualifiers

FT CDS 2..660

FT /*tag= a

FT /product= "partial MurC polypeptide"

PN EP-889123-A2.

PD 07-JAN-1999.

PF 26-JUN-1998; 305064.

PR 03-JUL-1997; US-052720.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Burnham MKR, Wallis NG;

DR WPI; 99-062655/06.

DR P-PSDB; W89199.

PT New isolated MurC polypeptide from Staphylococcus aureus and related
 PT nucleic acid - useful in diagnosis, treatment and prevention of
 PT bacterial infections

PS Claim 2; Pages 4-5; 39pp; English.

CC The invention relates to a UDP-N-acetylmuramate:L-alanine ligase
 CC (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells
 CC containing an expression system comprising the MurC gene can be used for
 CC the recombinant production of the polypeptide. Agonists or the MurC
 CC polypeptide are used to treat conditions requiring increased activity or
 CC expression of the polypeptide. Antagonists, inhibitory nucleic acid or
 CC competitive polypeptide are useful for inhibiting the polypeptide e.g.
 CC Helicobacter pylori infections and related cancers, ulcers and gastritis.

CC The antibacterial agents are useful to treat in-dwelling devices for
 CC infection prevention or generally as wound treatments to prevent adhesion
 CC of bacteria to matrix proteins. The MurC polypeptide is also useful for
 CC diagnosing or prognosing a (susceptibility to) disease, for raising
 CC antibodies; to identify modulators or specific receptors; in rational
 CC drug design and as an immunogen for vaccines. The MurC gene sequences are
 CC useful in antisense/ribozyme therapeutics; to detect mutant MurC gene;
 CC for chromosomal mapping; to determine bacterial serotype; and for genetic
 CC immunisation. The present sequence represents a partial nucleotide
 CC sequence (MurC ORF) of the MurC gene.

SQ Sequence 660 BP; 233 A; 120 G; 224 T;

Query Match 96.0%; Score 2557; DB 60; Length 660;

Best Local Similarity 59.4%; Pred. No. 9,998-211;

Matches 383; Conservative 157; Mismatches 105; Indels 0; Gaps 0;

Db 2 tttaaagattcgatgacattttatgctcaaaattacacgataaaggtagctgt 61

QY 1 TTYAARGAWSNGAYGAYATHYAGCNCARATHYTCARATHACNGAYAARGNACNGCN 60

Db 62 ttgtatgtatgtggtgagttttatgatcacttctctccacaattatggtgac 121

QY 61 GTNGAYGTNTAYGTNGAYGNGARTTYTAYGAYCAVTTYTNWSNCCNARTAYGNGAY 120

Db 122 catacagttttaaattcattagctgaattgagtagtatttagagaagtagatgtt 181

QY 121 CAYACNGTNTNAYGNGTNGCNGTNGCNGTNGTNGTNGTNGTNGTNGTNGTNGTNG 180

Db 182 acaaaattaaagaacattagaaacgtttgtgtggttaaacgtcttcaatgaact 241

QY 181 ACNAAATHAARGARCNCTNGARACNTTYGNGGNGTNGTNGTNGTNGTNGTNGTNGTNG 240

Db 242 acaattgcaatacaagttatttagatgattatgcacaccatcccaagaagaattagtt 301

QY 241 ACNATHGCAACARGTATGTHGTNGAYGAYTAYGNCAYCAYCCNMGNGARATHWSN 300

Db 302 acaattgcaacagcagaagaataatcacataaagaagttgttgagtagtattcaacca 361

QY 301 ACNATHGAYACNGCNGMNGNARARTAYCCNAYARGARTNGTNGCNGTNTTYCARCCN 360

Db 362 cacacttctctagacacacagcatttttaattgaattgagagaatttatgataagca 421

QY 361 CAYACNTTWSNMGNCARCNCTTYTNTNAYGARTTYGNCNGARWSNTNWSNARCN 420

[illegible]

DR EMBL: D09016; G1653723; -
KW PEPIDIOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
KW ATP-BINDING. 164 170 ATP (POTENTIAL).
SQ NP_BIND 505 AA; 54513 MW; B3D7FC7C CRC32;
Query Match .. 4.6%; Score 309; DB 1; Length 505;

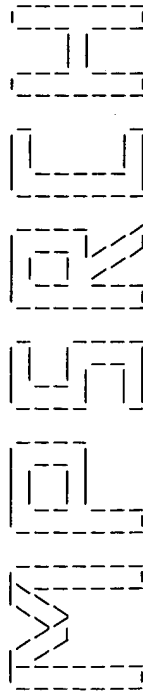
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Db	1081	GGNGCAGATG	GTNTAYTTC	GYATTTTG	GCNMGNS	CNCMNGA	RAAYG	CNGNGNAAR	1140												
Dt			: :	: :	: :	: :	: :	: :													
Qy	1102	AKACAGATG	CTGTATTG	TATGTAAT	TTTTGGCT	CAATTAG	AAGAAAT	CTCGGCCA	1161												
Qt		K A D R V F L C E I F G S I R E N S G A																			
Db		L T I G D L Q G K I H N A K L I E E D D																			
Dt	1141	YTACNATHG	GNAYTNC	ARGNNAAR	ATHCAYA	AGCNNAARY	TNATHGAR	GARGAYGAY	1200												
Qy		: :	: :	: :	: :	: :	: :	: :													
Qt	1162	TTAACGATA	CAAGAATT	TAATGATA	AAATGG	AGGTGCAT	CGTTCAAT	TAATGAAGATCTT	1221												
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Dt		T S V L K A H D K A V L I F M G A G D I																			
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Qt		: :	: :	: :	: :	: :	: :	: :													
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Qt		Q K																			
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Qt		Q K																			

RESULT 3
ID MURC-PORGI STANDARD; PRT: 433 AA.

AC Q51831:
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE UDP-N-ACETYLMURAMATE--ALANINE LIASE (EC 6.3.2.8) (UDP-N-
DE ACETYLMURAMOYL-L-ALANINE SYNTHETASE).
GN MURC.
OS PORPHYROMONAS GINGIVALIS (BACTEROIDES GINGIVALIS).
OC BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; PORPHYROMONAS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=381;
RX MEDLINE; 96118684.
RA ANSAI T., YAMASHITA Y., AWANO S., SHIBATA Y., WACHI M., NAGAI K.,
RA TAKEHARA T.;
RA "A murC gene in Porphyromonas gingivalis 381.";
RL MICROBIOLOGY 141:2047-2052(1995).
RN [2]
RP REVISIONS.
RC STRAIN=381;
RA ANSAI T.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBBJ DATA BANKS.
CC -1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE -
CC ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE MURCDF FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or email to licensesh@isb-sib.ch).

of send an email to: -----
CC
CC
CC
EMBL; D84504; D102570; -----
DRK PEPIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
DDB ATP-BINDING.
KW NP_BIND 114 120 ATP (POTENTIAL).
FT SEQUENCE 433 AA; 4830 MW; 38C4714B CRC32;
SQ



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Nov 24 00:36:34 1999; MasPar time 19.53 Seconds
 896.452 Million cell updates/sec

Tabular output not generated.

Title: >US-09-103-287-2
 Description: (1-437) from US09103287.pep
 Perfect Score: 3121
 Sequence: 1 MTHYFVGKSGMSSLAQI.....GDIQKLNQYLDKLGKNAF 437

Scoring table: PAM 150
 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: pif60
 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 50.576; Variance 122.235; scale 0.414

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
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2	620	19.9	454	2	B70418	2.69e-77
3	602	19.3	481	2	C71338	2.58e-74
4	584	18.7	495	2	C71679	2.42e-71
5	581	18.6	468	2	H70201	7.56e-71
6	567	18.2	803	2	A71475	1.53e-68
7	529	16.9	475	2	E61485	2.60e-62
8	495	15.9	491	1	CEECAM	8.97e-57
9	470	15.1	505	2	S76722	9.98e-53
10	440	14.1	453	2	B64084	6.64e-48
11	424	13.6	457	2	S56459	2.39e-45
12	422	13.5	449	2	G64597	4.98e-45
13	409	13.1	449	2	B71917	5.81e-43
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16	177	5.7	457	2	I64184	1.93e-08
17	160	5.1	445	2	A71699	3.05e-06
18	158	5.1	505	2	S75968	5.45e-06
19	154	4.9	682	2	A69170	1.73e-05
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21	142	4.5	508	2	A70325	5.11e-04
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23	128	4.1	449	2	JC6560	2.23e-02

24	128	4.1	457	2	F69662	2.23e-02
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26	121	3.9	464	2	H70137	1.36e-01
27	118	3.8	451	2	D47691	2.90e-01
28	119	3.8	482	2	E70450	2.26e-01
29	120	3.8	598	2	D71127	1.75e-01
30	116	3.7	437	2	B64185	4.77e-01
31	111	3.6	121	2	S18067	1.62e+00
32	113	3.6	320	2	S33172	9.96e-01
33	111	3.6	432	2	H64383	1.96e+00
34	111	3.6	493	2	D64612	1.62e+00
35	108	3.5	143	2	E69065	3.30e+00
36	109	3.5	452	2	F64730	2.61e+00
37	109	3.5	585	2	C70330	2.61e+00
38	110	3.5	1558	2	B71603	2.05e+00
39	110	3.5	1670	2	S71551	2.05e+00
40	105	3.4	227	2	H64336	6.65e+00
41	106	3.4	374	2	S75646	5.28e+00
42	106	3.4	416	2	E69599	5.28e+00
43	106	3.4	447	2	D71812	5.28e+00
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45	105	3.4	758	2	S37855	6.65e+00

ALIGNMENTS

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DATE	Bacillus subtilis	
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#authors	17-Mar-1999	
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#journal	Nature (1997) 390:249-256	
#title	The complete genome sequence of the Gram-positive bacterium	
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REFERENCE S71000
#authors Varon, D.; Brody, M.S.; Price, C.W.
#journal Mol. Microbiol. (1996) 20:339-350
#title Bacillus subtilis operon under the dual control of the
general stress transcription factor sigma(B) and the
sporulation transcription factor sigma(H).
#cross-references MUID:96310371
#accession S71002
##molecule_type DNA
##residues 85-432 ##label VAR
##cross-references EMBL:L31845; NID:g556013; PID:g556014
##experimental_source strain 168, substrain Marburg
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GENETICS *Experimental* source strain 100, substrain M4B19g
#gene murC
FUNCTION
#pathway peptidoglycan biosynthesis
KEYWORDS ATP binding; cell division; cell wall; ligase; peptidoglycan biosynthesis
SUMMARY #length 432 #molecular-weight 48364 #checksum 5127

[illegible]

```

REFERENCE
#authors
  Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
  Lenox, A.L.; Graham, D.E.; Overbeek, R.; Sneed, M.A.;
  Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
  J.M.; Olson, G.J.; Swanson, R.V.
#journal
  Nature (1998) 392:353-358
#title
  The complete genome of the hyperthermophilic bacterium
  Aquifex aeolicus.
#cross-references
  MUID:98196666
#accession
  B70418
#status
  preliminary; nucleic acid sequence not shown;
  translation not shown
#molecule_type
  DNA
#residues
  1-454 #label AQF
#cross-references
  GB:AE000736; NID:g2983763; PID:g2983764; GB:AE000657
#experimental_source
  strain VF5
GENETICS
#gene
  murC
CLASSIFICATION
#superfamily
  UDP-N-acetylmuramate--alanine ligase
SUMMARY
#length
  454 #molecular-weight
  50893 #checksum
  2346
Query Match          19.9%; Score 620; DB 2; Length 454;
Best Local Similarity 30.8%; Pred. No. 2 69e-77;
Matches 139; Conservative 125; Mismatches 164; Indels 24; Gaps 20;

Db 6 IKKPHFIGIGMGSIAQLLEMGYKVSQSDISENKNKTL-LKQGAKIYIGHRPNLG 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1 MTHYHFVGKSGMSLAQIMHDLGHEVGQSDIENYVFTEVALRNKGI-LPFGANNIK 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 65 DAQVYVSSAVKPNPPIQAKARNTPVPRGMLAELFKLEGIAVSGSHGKTTTSMI 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 60 EDMVVIQGNAPASHEBIEIRAHLKLDVSYNDFLQIIDQVTSVAVTGAHGKTTSTGL 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 125 AEILINAGLEPTVIIGRLKRIQTNAKLGRGELLVSEADESDGSLKLOPAVAIVNDR 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 120 SHVM-NGDKTSTFLIGD-----GTGMLPESDIFAFACEYRRHFUSYKPDVAIMTNDF 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 185 EHLDFYENFERVKEAFQFMNSVPFYGFVAVNLDPTLAQLVKKSHERVITYGINSPLV 244
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 174 DHPDYFDKINDVDAFQEMAHNVKK-GI-IAWGDDEHLRK-IE-ADVPIYYGFRKSDDI 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 245 RAKNLYLKEGRYEGVEFKGKELGRHLGTA-GIHNVYNALAAATGVA-IE-LGVSFVNIK 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 230 YAQNIQITDRGTAFDVYVGEFYDHF-LSPQYGDHTVNLALAVIAISYLEKLDVT-N-IK 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 302 KSLSEFRNARERLELGGYKNSPVDDYGHHPPEIKAVINSLRDMYDPKXNLLVQPHRY 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 287 EALETFGGKRRNETTI-ANQVIVDDYIAHHPREISATIDTARKYPHKVEVAVPQHTF 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 362 SRYLYLPEDEVKVLKQIDKLIVTDIYPAGENNVYGVSAEELARK-SCAVFAKDKVEPEK 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 346 SRTOAFLNEFAESLCRADRVFLCEIFGSTRNSGALTIQDLDKIGGASFI-N-EDLIN- 402
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 421 VREVHDDGDVILFLGAGSISKWCCEFLKEVNL 452
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 403 VLQSFQDNA-VVLEFMGAGDIQKLNQAYLDKGLM 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT	3
ENTRY	C71338
TITLE	#type complete probable UDP-N-acetylmuramate-alanine ligase (murC) - syphilis spirochete
ORGANISM	#formal_name Treponema pallidum subsp. pallidum #common_name syphilis spirochete
DATE	24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999
ACCESSIONS	C71338
REFERENCE	A11250
#authors	Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayton, R.; Kechum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Childambaram, M.; Utterback T.; McDonald


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/protein_id="AAB87090.1"
/db_xref="PID:g2642659"
/db_xref="GI:2642659"
/translation="MTHYFHYIKSGMSSLAQIMHIDIGHEVQSGDIENYVTFEVALR
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SVATVGAHGKTSTGLSHVNGDKTSLFDGTMGLPESDYFAEACERHFLS
YKPDYAIMNIDFDPDYFKDINDVDAFOEMAHNVKGIITAMGDDSHLRIEADVP
YYGFKSDDLIYAQNIQIDKGTAFDYVDGEFYDHELSPOYGHTVILNALAVIAY
LEKLDVNIKALSTFGGVKRRNETTIANQYVDDIAHHPREISATYARKKYPHK
EVAVFOPHTSRFOALNEFAESLRADRVFLCEIFGSIRESNTGALTIODLIDKIEG
ASLINEIDSNVLEQFADNAVLEKFGAGDIQKLNAYLDKLGKNAF"
BASE COUNT 467 a 163 c 250 g 434 t
ORIGIN

Query Match 96.6%; Score 2573; DB 17; Length 1314;
Best Local Similarity 59.5%; Pred. No. 8,76e-275;
Matches 384; Conservative 158; Mismatches 103; Indels 0; Gaps 0;

Db 667 TTAAAGATTGGGATGACATTTATGCTCAAAATATTCAAATTCACGATAAAGGTACTGCT 726
Qy 1 TTYAARGAYWSNGAYGAYATHYACNCARATHYTCARATHACNGAYAAAGNACNGCN 60

Db 727 TTGTAGTGTATGCGATGCGTGGTATTTATGATCATCTCTCTCCCAATATGCTGAC 786
Qy 61 GTNGAYGTNTAYGTNGAYGNGARTTYTAGYACATYTYTNWSNCCNARTAYGNGAY 120

Db 787 CATACAGTTTAAATGCATTAGCTGATATTCGGATAGTATTATAGAGAAGCATGATGTT 846
Qy 121 CAYACNGNTNNAAYGCGNTNGCNGTATGNCNATHWSNTAYTYNGARAARYNGAYGN 180

Db 847 ACAATATATAAGAACGATTCAGAACGTTTGGTGGTGTAAACGTCGTTTCAATGAACAT 906
Qy 181 ACNAYATHAARGAGCNGTNGARACNTTYGGNGGNGTNRARWNGMTTYTAAYGARACN 240

Db 907 ACAATGCAATCAAGTATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
Qy 241 ACNATHGCAATCAAGTATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

Db 967 ACAATGCAATCAAGTATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
Qy 301 ACNATHGCAATCAAGTATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

Db 1027 CACACTTCTCTAGAACACACAGCATTTTAAATGAATTCGAGAAAGTTAAGTAAACGA 1086
Qy 361 CAYACNTTYWSNMGACNACAGCNGTNTYTAAGARTTYGNGAGRTNGTNGCNGTNTTTCAR 420

Db 1087 GATCGTGATTCCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146
Qy 421 GAYMGNGTNTYTYNGYGARATHYTYGNGSNATHMGNGARAYACNGGNGCNYTNACN 480

Db 1147 ATACAGATTTAATGATAAATGAAGTGCATCGTGTATTAATGAAGATTCATTATTA 1206
Qy 481 ATHCARGAYTNTATHGAYAAATHGARGGNGCNSNTYTNATHAAYGARGAYWSNATHAAY 540

Db 1207 GTATTAGAACATTTGATAATGCTGTTGTTTATTAAGGCGTGCAGGTGATTCACAAA 1266
Qy 541 GTNTNGARCARTTYGATTAATGCGNGTNTNTYTAAGGCGGNGGNGAYATHCARAA 600

Db 1267 TTACAAATGCATATTTAGATAAATTAGGCATGAAATGCGTTT 1311
Qy 601 YTNCAAAAGCTAYTYNGAYAAATYNGGNTAGTAARAYGCTTY 645

RESULT 2
LOCUS BACUNAM 2320 bp DNA BCT 26-MAR-1997
DEFINITION Bacillus subtilis UDP-N-acetylmuramate-alanine ligase gene, partial cds, and 3 ORF's.
ACCESSION L31845
NID 9556013
VERSION L31845.1 GI:556013
KEYWORDS UDP-N-acetylmuramate:L-alanine ligase.
SOURCE Bacillus subtilis.
ORGANISM Bacillus subtilis
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BASE COUNT		750 a		464 c		549 g		557 t	
ORIGIN									
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<p>Query Match 49.2%; Score 1309; DB 17; Length 2320; Best Local Similarity 45.2%; Pred. No. 3.43e-125; Matches 272; Conservative 123; Mismatches 207; Indels 0; Gaps 0;</p>									
Db	430	ATGATTTTCAAGCGAACAACATCGTAAAGAAGCAGGAGGAGCAACTTTTGATGCTCTTG	489						
QY	14	AYGAVATHTAAGTCARATHTTTCARATHACNCAAGAAAGGACGTCGATGATGATG	73						
Db	490	TCGCAATACGTTCTATGATACGTTTATTCCTGCGTACGCGCACACACATGATTA	549						
QY	74	TGAYGGNGARITTYTAIGAYCATITTYTWSGCCNCAATAYGGNGAYCAYACNGTNT	133						
Db	550	ACTCATTCGGGCTCATTCGCTTATGCAATATGAAGAATGATCCAGCATTAAGC	609						
QY	134	AYCNYTNGCNGTATHGNCNATHWSNTAYTNGARAATNGAYTNGACNATYATHA	193						
Db	610	ATGCTCTCAATCTTTGGGGCGTCAACGAGCATTCATGAGAGCAGCGTGGGATC	669						
QY	194	ARGCNTNGARACNTTYGGNGGNGTNAARMGNGMTTYAAYCARACNACNATHG	253						
Db	670	AAGTGTGATTCATGACTATGCCATCCATCCGACAGAAATAAAGTGACATCGAG	729						
QY	254	ARGTNATHGTNGAYTAIGNCAYCAAYCCNMGNAGATHWSNGCNACNATHGAY	313						
Db	730	CAAGCAGAAAGTATCTGATCGGAAATGTCGCGGTATTCAGCGCTCATACATTT	789						
QY	314	CNMGNAARAARTAYCCNCAAYARGARGINGTCGTTTCARCCNCAACNTTYS	373						
Db	790	GGAGCAGCAGTTCCTTGACGAATTTGCAAGAAAGCCTGAGCGGCGGCGAGCT	849						
QY	374	GNACNARGCNTTYTNAAYGARTTYGCGNGARWSNYTWNAAAGCNGAYMGNGT	433						
Db	850	TATGCGATATTTTCGCTCAGCCGCTGAGATGCGGGAAGCTGACGATCGGTAT	909						
QY	434	TNTGYGARTHTTYGGNWSNATHMGNGARAYACNGGNCNTYACNATHCARGAY	493						
Db	910	AGGGAATATTCATATGCAAGCAGTATGGAAGAGATGACACATCTCTTTTAA	969						
QY	494	THGAYARAATHARGGNGCWNYSNTATHAAYGARGATWSNATHAAYTNTNGAR	553						
Db	970	ATGATAAGCCGTTCTCATCTTCATGTTGGGAGCAGGAGATATCAAAAATAT	1029						
QY	554	TYGAYAAAYCNGTNGTNTNTTYATGGGNGGNGGAYATHCARAARYTNCARA	613						
Db	1030	AC 1031							
QY	614	AY 615							
<p>RESULT 3 LOCUS BSUB0016 215640 bp DNA BCT 26-NOV-1997 DEFINITION Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410. ACCESSION Z991119 AL009126 NID 92635411 VERSION Z99119.1 GI:2635411 KEYWORDS SOURCE Bacillus subtilis. ORGANISM Bacillus subtilis Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae; REFERENCE 1 (bases 1 to 215640) AUTHORS Kunst,F., Ogasawara,N., Moszer,I., Albertini,A.M., Alloni,G., Azevedo,V., Bertero,M.G., Bessieres,P., Bolotin,A., Borchert,S., Borriss,R., Boursier,L., Brans,A., Braun,M., Brignell,S.C.,</p>									

QY 61 TNIKEALETFGGVKKRRFNETTIANQIVDDYAHHPREISATIDTARKKYPHKEVAVFOP 120
 Db 343 HTFSRTOAFLEFAESLSKADRVFLCEIFGSRNTGALTIODLIDKIEGASLINEDSN 402
 QY 121 HTFSRTOAFLEFAESLSKADRVFLCEIFGSRNTGALTIODLIDKIEGASLINEDSN 180
 Db 403 VLEQFDNAVFLFKGAGDIQKQYAYLDKLGKNAF 437
 QY 181 VLEQFDNAVFLFKGAGDIQKQYAYLDKLGKNAF 215
 RESULT 2
 ID MURC_BACSU STANDARD; PRT; 432 AA.
 AC P40778;
 DT 01-FEB-1995 (REL. 31, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE UDP-N-ACETYLURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
 ACETYLURAMOYL-L-ALANINE SYNTHETASE).
 GN MURC
 OS BACILLUS SUBTILIS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98048467.
 RA LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH S.D.;
 RT "Sequencing and functional annotation of the Bacillus subtilis genes
 in the 200 kb rnb-dnaB region.";
 RL MICROBIOLOGY 143:3431-3441(1997).
 RP SEQUENCE OF 85-432 FROM N.A.
 RC STRAIN-168 / MARBURG;
 RX MEDLINE; 96310371.
 RA VARON D., BRODY M.S., PRICE C.W.;
 RT "Bacillus subtilis operon under the dual control of the general
 stress transcription factor sigma B and the sporulation transcription
 factor sigma H";
 RL MOL. MICROBIOL. 20:339-350(1996).
 CC -1- FUNCTION: CELL WALL FORMATION.
 CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLURAMOYL-L-ALANINE -
 ADP + ORTHOPHOSPHATE + UDP-N-ACETYLURAMOYL-L-ALANINE -
 -1- SUBCELLULAR LOCATION: BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE MURDEF FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 DR EMBL; AF008220; G2293216;
 DR EMBL; L31845; G356014;
 DR SUBTILIST; BG10973; MURC.
 KW PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
 NP_BIND 108 114
 FT ATP-BINDING.
 SQ SEQUENCE 432 AA; 48364 MW; 163166CB CRC32;
 Query Match 57.7%; Score 863; DB 1; Length 432;
 Best Local Similarity 59.1%; Pred. No. 1.20e-132;
 Matches 120; Conservative 32; Mismatches 51; Indels 0; Gaps 0;
 Db 225 EENDFOARNIVKSTEGTDFVFRNTFDYFYIPAYGHVNLAVIALCHYEIDSSI 284
 QY 3 DSDIYIAQIFQIDKGTAVDYYDGEYDFLSPQGDHTVNLAVIALSYLEKLDVTN 62
 Db 285 IKHALSFGVKRRFNEKQGLDQVLDYAHHPREISATIDTARKKYPHKEVAVFOPHT 344
 QY 63 IKALETFGVKKRRFNETTIANQIVDDYAHHPREISATIDTARKKYPHKEVAVFOPHT 122

Db 345 FTRTOQFLDEFAESLSGADCVVLCDFGSARENAACKLTIGDLOGKIHNAKIEEDTSVL 404
 QY 123 FSRTQAFLEFAESLSKADRVFLCEIFGSRNTGALTIODLIDKIEGASLINEDSN 182
 Db 405 KAHDKAVLIFMGAGDIQKQYAYLDKLGKNAF 427
 QY 183 EQFDNAVFLFKGAGDIQKQYAYLDKLGKNAF 205

RESULT 3
 ID MURC_SINY3 STANDARD; PRT; 505 AA.
 AC P74528;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DE UDP-N-ACETYLURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
 ACETYLURAMOYL-L-ALANINE SYNTHETASE).
 GN MURC OR SLR1423.
 OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
 OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RL DNA RES. 3:109-136(1996).
 CC -1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLURAMOYL-L-ALANINE -
 ADP + ORTHOPHOSPHATE + UDP-N-ACETYLURAMOYL-L-ALANINE -
 -1- SUBCELLULAR LOCATION: BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE MURDEF FAMILY.
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 or send an email to license@isb-sib.ch).
 DR EMBL; D90916; G1653723;
 DR PEPTIDOGLYCAN SYNTHESIS; CELL WALL; CELL DIVISION; LIGASE;
 KW ATP-BINDING.
 NP_BIND 164 170
 FT ATP-BINDING.
 SQ SEQUENCE 505 AA; 54513 MW; B3D7FC7C CRC32;
 Query Match 22.9%; Score 343; DB 1; Length 505;
 Best Local Similarity 43.8%; Pred. No. 1.62e-37;
 Matches 57; Conservative 29; Mismatches 40; Indels 4; Gaps 4;
 Db 322 GDHNSNALAAVAVGRLLGLDFPVIAQAIASFNGAKRRFECKGVCNGITFIDYAHHPSE 381
 QY 39 GDHVTNLALAVIALSYLEKLDVTNKEALTFGGVKKRRFNETTIANQV-IVDDYAHHPRE 97
 Db 382 LLATLAAAKQVTHGYKRVVAIFQPHYSRTHTFMAEFATFKDADLVLTDIYSAGEQ 441
 QY 98 ISATIDTARKKYPH-K-E-VVAVFQPHYSRTHTFMAEFATFKDADLVLTDIYSAGEQ 441
 Db 442 NPYNIRGED 451
 QY 155 NTGALTIOQL 164

RESULT 4
 ID MURC_PORGI STANDARD; PRT; 433 AA.